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The new GeneChip® One-Cycle and
Two-Cycle cDNA Synthesis Kits.


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Full Record

Details for HUGENEFL:X15880_AT

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GeneChip Array Information

Probe Set ID X15880_at

GeneChip Array HumanGeneFL Array

Organism Common Name Human

Probe Design Information

Transcript ID X15880

Sequence Type Exemplar sequence

Representative Public ID X15880 NCBI

Target Description X15880, class C, 20 probes, 20 in all_X15880 1690-2273, Human mRNA for collagen VI alpha-1 C-terminal globular domain

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Position	% Identity	Cytoband
chr21: 46280561-46281145 (+) UCSC	100	q22.3

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
NM_001848	collagen, type VI, alpha 1	chr21:46257869-46281164 (+) UCSC	

Public Domain and Genome References

Gene Title collagen, type VI, alpha 1

Gene Symbol COL6A1 [HGNC](#)

Chromosomal Location 21q22.3

UniGene ID Hs.415997 [NCBI](#) (FULL LENGTH)

Ensembl ENSG00000142156 [Ensembl](#)

LocusLink 1291 [NCBI](#)

P12109 [EMBL-EBI](#)

Q7Z645 [EMBL-EBI](#)

Q8TBN2 [EMBL-EBI](#)

Q9BSA8 [EMBL-EBI](#)

OMIM 120220 [NCBI](#)

	RefSeq Protein ID	NP_001839 NCBI			
	RefSeq Transcript ID	NM_001848 NCBI	RefSeq Title	collagen, type VI, alpha 1 precursor	
Functional Annotations					
	ID	Title	Organism	Type	
Ortholog	MG-U74AV2:162459_F_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog	
	MG-U74AV2:95493_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog	
	MOE430A:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog	
	MU11KSUBB:X66405_S_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog	
	MOUSE430_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog	
	MOUSE430A_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog	
GO Biological Process (view graph)					
	ID	Description	Evidence	Links	
Gene Ontology	7155	cell adhesion	non-traceable author statement	QuickGO AmiGO	
	GO Cellular Component (view graph)				
	ID	Description	Evidence	Links	
	5578	extracellular matrix	inferred from electronic annotation	QuickGO AmiGO	
	5589	collagen type VI	non-traceable author statement	QuickGO AmiGO	
	GO Molecular Function (view graph)				
	ID	Description	Evidence	Links	
Protein Similarities	5194	cell adhesion molecule activity	inferred from electronic annotation	QuickGO AmiGO	
	5201	extracellular matrix structural constituent	inferred from electronic annotation	QuickGO AmiGO	
	Method	ID	Description	E-Value	
	blast	15011913		0.0	
	blast	13878903		0.0	
	Database	ID	Description	E-Value	
Protein Domains	scop	d1atza	d1atza_SCOP:c.62.1.1:1 von Willebrand factor A3 domain	3.63E-37	
	pfam	vwa	von Willebrand factor type A domain	9.6E-24	
	pfam	vwa	von Willebrand factor type A domain	4.7E-32	
	pfam	vwa	von Willebrand factor type A domain	2.7E-35	
	pfam	Collagen	Collagen triple helix repeat (20 copies)	2.4E-11	
	pfam	Collagen	Collagen triple helix repeat (20 copies)	3.8E-14	
	pfam	Collagen	Collagen triple helix repeat (20 copies)	3.3E-10	
	pfam	Collagen	Collagen triple helix repeat (20 copies)	2.6E-11	
	InterPro	IPR008161	Collagen helix repeat		
	InterPro	EMBL-EBI			
	InterPro	IPR002035	von Willebrand factor, type A		
	InterPro	EMBL-EBI			

InterPro IPR008160 Collagen triple helix repeat
EMBL-EBI

Sequence					
Target Sequence	>HUGENEFL:X15880_AT				
	agcaagacgcctcggggctgtgccgactagccctccctgtccccatagct ggttttcccaccaatcctcacctaacagttacttacaattaaactcaaagcaagctct tctccctagctggggcagccattggctctgtctcggtttggaaaccaaggtcaggag gccgttgacagacataaatctcgcgactcggccccgtctcctgagggtcgtgggtac cggcctggacctggccctacagccctggaggccgtgtgaccagcactgaccggccacc tcagagagtactcgcagggggcgtggctgcactcaagaccctcgagattaacgggtctaa ccccgtctgctcctccctcccgacagactggggcgtggactggacatgagagcccccttg gtgccacagaggcgtgtttactagaaaacaacgaaacctctcctcagaatagt gatgtgttcgacgttttatcaaaggcccccttctatgttcatgttagtttgctccttc tgtgtttttctgaaccatatccatgttgactttccaa				
Probe Info	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Position	Interrogation Strandedness
	AGCAAGACGCCTCTCGGGGCCTGTG	76	317	1702	Antisense
	AAACTCAAAGCAAGCTTCTCCTC	77	317	1804	Antisense
	AAAGCAAGCTTTCTCCTCAGCTTG	78	317	1810	Antisense
	TCTCCTCAGCTTGGGGCAGCCATTG	79	317	1822	Antisense
	GCCATTGGCCCTGTCTCGTTTGG	80	317	1840	Antisense
	GCAGACATAATCTCGGCGACTCGG	81	317	1888	Antisense
	GCCCCGTCTCCTGAGGGTCTGCTG	82	317	1912	Antisense
	TGGCCCTACAGCCCTGGAGGCCGCT	83	317	1954	Antisense
	TCAGAGAGTACTCGCAGGGGCGCTG	84	317	2002	Antisense
	AGTACTCGCAGGGGCGCTGGCTGCA	85	317	2008	Antisense
	GGCGCTGGCTGCACTAAGACCCTC	86	317	2020	Antisense
	GGACATGAGAGCCCCCTGGTGCCAC	87	317	2104	Antisense
	GAGAGCCCCCTGGTGCCACAGAGGG	88	317	2110	Antisense
	CCCTTGGTCCCACAGAGGGCTGTGT	89	317	2116	Antisense
	GTGCCACAGAGGGCTGTGTCTTACT	90	317	2122	Antisense
	CAGAGGGCTGTGTCTTACTAGAAC	91	317	2128	Antisense
	CTCCTTCCTCAGAATAGTGTGTGT	92	317	2164	Antisense
	TTTTCTGAACCATATCCATGTTGC	93	317	2248	Antisense
	TGAACCATATCCATGTTGCTGACTT	94	317	2254	Antisense
	ATATCCATGTTGCTGACTTTCCAA	95	317	2260	Antisense